



## SEQUENCE LISTING

<100> Zastawny, Roman

<120> G PROTEIN COUPLED RECEPTOR A4

<130> 2931-104

<140> US 10/060369

<141> 2002-02-01

<150> US 09/173565

<151> 1998-08-16

<160> 12

<170> PatentIn version 3.2

<210> 1

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 1

gagacataat ggtgatggct aggaccca

28

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<212> DNA

<213> Artificial Sequence

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<223> PCR primer

<400> 2

ctgcgacaga tattccctgg accaatcc

28

<210> 3

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> PCR primer

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ccatcctaatac gactcact ataggc

26

<210> 4

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actcactata gggctcgagc ggc

23

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ggcattcgaa ttcgccgcca ccatgaatga gaaatgggac acaaactctt

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aggattatca ctctagatct ttttaaactct cactgctggt agtagtttct

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tggcacgtgg tgtccaggaa gaagcag

27

<210> 8  
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<213> Human

<400> 8  
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60

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atgaatgaga aatgggacac aaactcttca gaaaactggc atcccatctg gaatgtcaat 180  
gacacaaagc atcatctgta ctgagatatt aatattacct atgtgaacta ctatcttcac 240  
cagcctcaag tggcagcaat cttcattatt tcctactttc tgatcttctt tttgtgcatg 300  
atgggaaata ctgtgggttg ctttattgta atgaggaaca aacatatgca cacagtcact 360  
aatctcttca tcttaaacct ggccataagt gatttactag ttggcatatt ctgcatgcct 420  
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gaagcttata ccctaaaagc taaaagccat gtgctcataa acacatctaa tcagcttgct 1260  
caggaatcta catttcaaaa cctcatggg gaaaccttgc tttataggaa aagtgtgaa 1320  
aaacccaac aggaattagt gatggaagaa ttaaaagaaa ctactaacag cagtgagatt 1380  
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<212> PRT  
<213> Human

<400> 9

Met Asn Glu Lys Trp Asp Thr Asn Ser Ser Glu Asn Trp His Pro Ile

1

5

10

15

Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp Ile Asn Ile  
20 25 30

Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala Ala Ile Phe  
35 40 45

Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met Gly Asn Thr  
50 55 60

Val Val Cys Phe Ile Val Met Arg Asn Lys His Met His Thr Val Thr  
65 70 75 80

Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu Val Gly Ile  
85 90 95

Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala Gly Trp Pro  
100 105 110

Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu Val Gln Gly Ile Ser  
115 120 125

Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Asp Arg Phe  
130 135 140

Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile Lys Thr Ala  
145 150 155 160

Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr Ile Met Ser  
165 170 175

Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr Tyr Arg Val  
180 185 190

Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp Cys Arg Glu  
195 200 205

Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr Val Leu Phe  
210 215 220

Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile Met Tyr Gly  
 225 230 235 240

Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His Thr Gly Arg  
 245 250 255

Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys Gln Lys Ile  
 260 265 270

Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu Ser Trp Leu  
 275 280 285

Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp Leu Ser Pro  
 290 295 300

Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe Ala His Trp  
 305 310 315 320

Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr Gly Phe Phe  
 325 330 335

Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln Leu Gln Leu  
 340 345 350

Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Thr Leu Lys Ala Lys  
 355 360 365

Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln Glu Ser Thr  
 370 375 380

Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys Ser Ala Glu  
 385 390 395 400

Lys Pro Gln Gln Glu Leu Val Met Glu Glu Leu Lys Glu Thr Thr Asn  
 405 410 415

Ser Ser Glu Ile  
 420

<210> 10  
 <211> 384  
 <212> PRT

&lt;213&gt; Human

&lt;400&gt; 10

Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val His Ser  
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Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn Asp Asp  
 20 25 30

Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala Tyr Gly  
 35 40 45

Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile  
 50 55 60

Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val  
 65 70 75 80

Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu Pro Phe  
 85 90 95

Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Ala Met  
 100 105 110

Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile  
 115 120 125

Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn  
 130 135 140

Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly Ile Ala  
 145 150 155 160

Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr  
 165 170 175

Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr  
 180 185 190

Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg  
 195 200 205

Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu  
 210 215 220

Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg  
 225 230 235 240

Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser  
 245 250 255

Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe  
 260 265 270

Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp  
 275 280 285

Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu  
 290 295 300

Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr  
 305 310 315 320

Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn  
 325 330 335

Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met  
 340 345 350

Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser  
 355 360 365

Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn Glu Lys Ile  
 370 375 380

<210> 11  
 <211> 444  
 <212> PRT  
 <213> Human

<400> 11

Met Ser Gly Thr Lys Leu Glu Asp Ser Pro Pro Cys Arg Asn Trp Ser  
 1 5 10 15

Ser Ala Ser Glu Leu Asn Glu Thr Gln Glu Pro Phe Leu Asn Pro Thr  
 20 25 30

Asp Tyr Asp Asp Glu Glu Phe Leu Arg Tyr Leu Trp Arg Glu Tyr Leu  
 35 40 45

His Pro Lys Glu Tyr Glu Trp Val Leu Ile Ala Gly Tyr Ile Ile Val  
 50 55 60

Phe Val Val Ala Leu Ile Gly Asn Val Leu Val Cys Val Ala Val Trp  
 65 70 75 80

Lys Asn His His Met Arg Thr Val Thr Asn Tyr Phe Ile Val Asn Leu  
 85 90 95

Ser Leu Ala Asp Val Leu Val Thr Ile Thr Cys Leu Pro Ala Thr Leu  
 100 105 110

Val Val Asp Ile Thr Glu Thr Trp Phe Phe Gly Gln Ser Leu Cys Lys  
 115 120 125

Val Ile Pro Tyr Leu Gln Thr Val Ser Val Ser Val Ser Val Leu Thr  
 130 135 140

Leu Ser Cys Ile Ala Leu Asp Arg Trp Tyr Ala Ile Cys His Pro Leu  
 145 150 155 160

Met Phe Lys Ser Thr Ala Lys Arg Ala Arg Asn Ser Ile Val Ile Ile  
 165 170 175

Trp Ile Val Ser Cys Ile Ile Met Ile Pro Gln Ala Ile Val Met Glu  
 180 185 190

Cys Ser Thr Val Phe Pro Gly Leu Ala Asn Lys Thr Thr Leu Phe Thr  
 195 200 205

Val Cys Asp Glu Arg Trp Gly Gly Glu Ile Tyr Pro Lys Met Tyr His  
 210 215 220

Ile Cys Phe Phe Leu Val Thr Tyr Met Ala Pro Leu Cys Leu Met Val  
 225 230 235 240



Leu Ala Tyr Leu Gln Ile Phe Arg Lys Leu Trp Cys Arg Gln Ile Pro  
 245 250 255

Gly Thr Ser Ser Val Val Gln Arg Lys Trp Lys Pro Leu Gln Pro Val  
 260 265 270

Ser Gln Pro Arg Gly Pro Gly Gln Pro Thr Lys Ser Arg Met Ser Ala  
 275 280 285

Val Ala Ala Glu Ile Lys Gln Ile Arg Ala Arg Arg Lys Thr Ala Arg  
 290 295 300

Met Leu Met Val Val Leu Leu Val Phe Ala Ile Cys Tyr Leu Pro Ile  
 305 310 315 320

Ser Ile Leu Asn Val Leu Lys Arg Val Phe Gly Met Phe Ala His Thr  
 325 330 335

Glu Asp Arg Glu Thr Val Tyr Ala Trp Phe Thr Phe Ser His Trp Leu  
 340 345 350

Val Tyr Ala Asn Ser Ala Ala Asn Pro Ile Ile Tyr Asn Phe Leu Ser  
 355 360 365

Gly Lys Phe Arg Glu Glu Phe Lys Ala Ala Phe Ser Cys Cys Cys Leu  
 370 375 380

Gly Val His His Arg Gln Glu Asp Arg Leu Thr Arg Gly Arg Thr Ser  
 385 390 395 400

Thr Glu Ser Arg Lys Ser Leu Thr Thr Gln Ile Ser Asn Phe Asp Asn  
 405 410 415

Ile Ser Lys Leu Ser Glu Gln Val Val Leu Thr Ser Ile Ser Thr Leu  
 420 425 430

Pro Ala Ala Asn Gly Ala Gly Pro Leu Gln Asn Trp  
 435 440

<210> 12

<211> 428  
 <212> PRT  
 <213> Human

<400> 12

Met Asp Val Val Asp Ser Leu Leu Val Asn Gly Ser Asn Ile Thr Pro  
 1 5 10 15

Pro Cys Glu Leu Gly Leu Glu Asn Glu Thr Leu Phe Cys Leu Asp Gln  
 20 25 30

Pro Arg Pro Ser Lys Glu Trp Gln Pro Ala Val Gln Ile Leu Leu Tyr  
 35 40 45

Ser Leu Ile Phe Leu Leu Ser Val Leu Gly Asn Thr Leu Val Ile Thr  
 50 55 60

Val Leu Ile Arg Asn Lys Arg Met Arg Thr Val Thr Asn Ile Phe Leu  
 65 70 75 80

Leu Ser Leu Ala Val Ser Asp Leu Met Leu Cys Leu Phe Cys Met Pro  
 85 90 95

Phe Asn Leu Ile Pro Asn Leu Leu Lys Asp Phe Ile Phe Gly Ser Ala  
 100 105 110

Val Cys Lys Thr Thr Thr Tyr Phe Met Gly Thr Ser Val Ser Val Ser  
 115 120 125

Thr Phe Asn Leu Val Ala Ile Ser Leu Phe Arg Tyr Gly Ala Ile Cys  
 130 135 140

Lys Pro Leu Gln Ser Arg Val Trp Gln Thr Lys Ser His Ala Leu Lys  
 145 150 155 160

Val Ile Ala Ala Thr Trp Cys Leu Ser Phe Thr Ile Met Thr Pro Tyr  
 165 170 175

Pro Ile Tyr Ser Asn Leu Val Pro Phe Thr Lys Asn Asn Asn Gln Thr  
 180 185 190

Ala Asn Met Cys Arg Phe Leu Leu Pro Asn Asp Val Met Gln Gln Ser

195		200		205
Trp His Thr Phe Leu Leu Leu Ile Leu Phe Leu Ile Pro Gly Ile Val				
210		215		220
Met Met Val Ala Tyr Gly Leu Ile Ser Leu Glu Leu Tyr Gln Gly Ile				
225		230		235 240
Lys Phe Glu Ala Ser Gln Lys Lys Ser Ala Lys Glu Arg Lys Pro Ser				
	245		250	255
Thr Thr Ser Ser Gly Lys Tyr Glu Asp Ser Asp Gly Cys Tyr Leu Gln				
	260		265	270
Lys Thr Arg Pro Pro Arg Lys Leu Glu Leu Arg Gln Leu Ser Thr Gly				
	275		280	285
Ser Ser Ser Arg Ala Asn Arg Ile Arg Ser Asn Ser Ser Ala Ala Asn				
	290		295	300
Leu Met Ala Lys Lys Arg Val Ile Arg Met Leu Ile Val Ile Val Val				
305		310		315 320
Leu Phe Phe Leu Cys Trp Met Pro Ile Phe Ser Ala Asn Ala Trp Arg				
	325		330	335
Ala Tyr Asp Thr Ala Ser Ala Glu Arg Arg Leu Ser Gly Thr Pro Ile				
	340		345	350
Ser Phe Ile Leu Leu Leu Ser Tyr Thr Ser Ser Cys Val Asn Pro Ile				
	355		360	365
Ile Tyr Cys Phe Met Asn Lys Arg Phe Arg Leu Gly Phe Met Ala Thr				
	370		375	380
Phe Pro Cys Cys Pro Asn Pro Gly Pro Pro Gly Ala Arg Gly Glu Val				
385		390		395 400
Gly Glu Glu Glu Glu Gly Gly Thr Thr Gly Ala Ser Leu Ser Arg Phe				
	405		410	415

[illegible]

Ser Tyr Ser His Met Ser Ala Ser Val Pro Pro Gln  
420 425